

OIPE

RAW SEQUENCE LISTING DATE: 01/04/2001
 PATENT APPLICATION: US/09/734,002 TIME: 09:37:13

Input Set : A:\seiki sequence listing.txt
 Output Set: N:\CRF3\01042001\I734002.raw

SEQUENCE LISTING

C--> 3 (1) GENERAL INFORMATION:
 5 (i) APPLICANT: Motoharu SEIKI et al.
 7 (ii) TITLE OF INVENTION: NOVEL PROTEIN AND MONOCLONAL ANTIBODY SPECIFIC THERETO
 9 (iii) NUMBER OF SEQUENCES: 14
 11 (iv) CORRESPONDENCE ADDRESS:
 12 (A) ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
 13 (B) STREET: 2033 K Street, N.W., Suite 800
 14 (C) CITY: Washington
 15 (D) STATE: D.C.
 16 (E) COUNTRY: U.S.A.
 17 (F) ZIP: 20006
 19 (v) COMPUTER READABLE FORM:
 20 (A) MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
 21 (B) COMPUTER: IBM Compatible
 22 (C) OPERATING SYSTEM: MS-DOS
 23 (D) SOFTWARE: Wordperfect 5.1
 30 (vi) CURRENT APPLICATION DATA:
 C--> 31 (A) APPLICATION NUMBER: US/09/734,002
 C--> 32 (B) FILING DATE: 12-Dec-2000
 33 (C) CLASSIFICATION:
 35 (vii) PRIOR APPLICATION DATA:
 C--> 36 (A) APPLICATION NUMBER: PCT/JP96/01956
 C--> 37 (B) FILING DATE: July 12, 1996
 C--> 39 (viii) ATTORNEY/AGENT INFORMATION:
 40 (A) NAME: Lee Cheng
 41 (B) REGISTRATION NUMBER: 40,949
 42 (C) REFERENCE/DOCKET NUMBER:
 44 (ix) TELECOMMUNICATION INFORMATION:
 45 (A) TELEPHONE: 202-721-8200
 46 (B) TELEFAX: 202-721-8250
 47 (C) TELEX:

Does Not Comply
 Corrected Diskette Needed
 See p. 2

ERRORED SEQUENCES

229 (2) INFORMATION FOR SEQ ID NO: 2:
 231 (i) SEQUENCE CHARACTERISTICS:
 232 (A) LENGTH: 607
 233 (B) TYPE: Amino acid
 234 (C) STRANDEDNESS: Single
 235 (D) TOPOLOGY: Linear
 237 (ii) MOLECULE TYPE: Protein
 239 (vi) ORIGINAL SOURCE:
 240 (A) ORGANISM: Human
 C--> 242 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 244 Met Ile Leu Leu Thr Phe Ser Thr Gly Arg Arg Leu Asp Phe Val His

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```

245 1           5           10           15
247 His Ser Gly Val Phe Phe Leu Gln Thr Leu Leu Trp Ile Leu Cys Ala
248           20           25           30
250 Thr Val Cys Gly Thr Glu Gln Tyr Phe Asn Val Glu Val Trp Leu Gln
251           35           40           45
253 Lys Tyr Gly Tyr Leu Pro Pro Thr Asp Pro Arg Met Ser Val Leu Arg
254           50           55           60
256 Ser Ala Glu Thr Met Gln Ser Ala Leu Ala Ala Met Gln Gln Phe Tyr
257 65           70           75           80
259 Gly Ile Asn Met Thr Gly Lys Val Asp Arg Asn Thr Ile Asp Trp Met
260           85           90           95
262 Lys Lys Pro Arg Cys Gly Val Pro Asp Gln Thr Arg Gly Ser Ser Lys
263           100          105          110
265 Phe His Ile Arg Arg Lys Arg Tyr Ala Leu Thr Gly Gln Lys Trp Gln
266           115          120          125
268 His Lys His Ile Thr Tyr Ser Ile Lys Asn Val Thr Pro Lys Val Gly
269           130          135          140
271 Asp Pro Glu Thr Arg Lys Ala Ile Arg Arg Ala Phe Asp Val Trp Gln
272 145          150          155          160
274 Asn Val Thr Pro Leu Thr Phe Glu Glu Val Pro Tyr Ser Glu Leu Glu
275           165          170          175
277 Asn Gly Lys Arg Asp Val Asp Ile Thr Ile Ile Phe Ala Ser Gly Phe
278           180          185          190
280 His Gly Asp Ser Ser Pro Phe Asp Gly Glu Gly Gly Phe Leu Ala His
281           195          200          205
283 Ala Tyr Phe Pro Gly Pro Gly Ile Gly Gly Asp Thr His Phe Asp Ser
284           210          215          220
286 Asp Glu Pro Trp Thr Leu Gly Asn Pro Asn His Asp Gly Asn Asp Leu
287 225          230          235          240
289 Phe Leu Val Ala Val His Glu Leu Gly His Ala Leu Gly Leu Glu His
290           245          250          255
292 Ser Asn Asp Pro Thr Ala Ile Met Ala Pro Phe Tyr Gln Tyr Met Glu
293           260          265          270
295 Thr Asp Asn Phe Lys Leu Pro Asn Asp Asp Leu Gln Gly Ile Gln Lys
296           275          280          285
298 Ile Tyr Gly Pro Pro Asp Lys Ile Pro Pro Pro Thr Arg Pro Leu Pro
299           290          295          300
301 Thr Val Pro Pro His Arg Ser Ile Pro Pro Ala Asp Pro Arg Lys Asn
302 305          310          315          320
304 Asp Arg Pro Lys Pro Pro Arg Pro Pro Thr Gly Arg Pro Ser Tyr Pro
305           325          330          335
307 Gly Ala Lys Pro Asn Ile Cys Asp Gly Asn Phe Asn Thr Leu Ala Ile
308           340          345          350
310 Leu Arg Arg Glu Met Phe Val Phe Lys Asp Gln Trp Phe Trp Arg Val
311           355          360          365
313 Arg Asn Asn Arg Val Met Asp Gly Tyr Pro Met Gln Ile Thr Tyr Phe
314           370          375          380
316 Trp Arg Gly Leu Pro Pro Ser Ile Asp Ala Val Tyr Glu Asn Ser Asp
E--> 317 375          390          395          400

```

Invalid amino acid number.
 Should be 385.

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```

319 Gly Asn Phe Val Phe Phe Lys Gly Asn Lys Tyr Trp Val Phe Lys Asp
320                               405 410 415
322 Thr Thr Leu Gln Pro Gly Tyr Pro His Asp Leu Ile Thr Leu Gly Ser
323                               420 425 430
325 Gly Ile Pro Pro His Gly Ile Asp Ser Ala Ile Trp Trp Glu Asp Val
326                               435 440 445
328 Gly Lys Thr Tyr Phe Phe Lys Gly Asp Arg Tyr Trp Arg Tyr Ser Glu
329                               450 455 460
331 Glu Met Lys Thr Met Asp Pro Gly Tyr Pro Lys Pro Ile Thr Val Trp
332 465                               470 475 480
334 Lys Gly Ile Pro Glu Ser Pro Gln Gly Ala Phe Val His Lys Glu Asn
335                               485 490 495
337 Gly Phe Thr Tyr Phe Tyr Lys Gly Lys Glu Tyr Trp Lys Phe Asn Asn
338                               500 505 510
340 Gln Ile Leu Lys Val Glu Pro Gly His Pro Arg Ser Ile Leu Lys Asp
341                               515 520 525
343 Phe Met Gly Cys Asp Gly Pro Thr Asp Arg Val Lys Glu Gly His Ser
344                               530 535 540
346 Pro Pro Asp Asp Val Asp Ile Val Ile Lys Leu Asp Asn Thr Ala Ser
347 545                               550 555 560
349 Thr Val Lys Ala Ile Ala Ile Val Ile Pro Cys Ile Leu Ala Leu Cys
350                               565 570 575
352 Leu Leu Val Leu Val Tyr Thr Val Phe Gln Phe Lys Arg Lys Gly Thr
353                               580 585 590
355 Pro Arg His Ile Leu Tyr Cys Lys Arg Ser Met Gln Glu Trp Val
356                               595 600 605

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VERIFICATION SUMMARY

DATE: 01/04/2001

PATENT APPLICATION: US/09/734,002

TIME: 09:37:15

Input Set : A:\seiki sequence listing.txt

Output Set: N:\CRF3\01042001\I734002.raw

L:3 M:220 C: Keyword misspelled or invalid format, [(1) GENERAL INFORMATION:]
 L:26 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
 L:27 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
 L:31 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
 L:32 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
 L:39 M:220 C: Keyword misspelled or invalid format, [(viii) ATTORNEY/AGENT INFORMATION:]
 L:36 M:220 C: Keyword misspelled or invalid format, (A) APPLICATION NUMBER:
 L:37 M:220 C: Keyword misspelled or invalid format, (B) FILING DATE:
 L:62 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
 L:242 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
 L:317 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
 L:370 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
 L:386 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
 L:401 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
 L:416 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
 L:432 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
 L:446 M:220 C: Keyword misspelled or invalid format, [(C) STRANDEDNESS:]
 L:447 M:220 C: Keyword misspelled or invalid format, [(D) TOPOLOGY:]
 L:451 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
 L:462 M:220 C: Keyword misspelled or invalid format, [(C) STRANDEDNESS:]
 L:463 M:220 C: Keyword misspelled or invalid format, [(D) TOPOLOGY:]
 L:467 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
 L:478 M:220 C: Keyword misspelled or invalid format, [(C) STRANDEDNESS:]
 L:479 M:220 C: Keyword misspelled or invalid format, [(D) TOPOLOGY:]
 L:483 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
 L:494 M:220 C: Keyword misspelled or invalid format, [(C) STRANDEDNESS:]
 L:495 M:220 C: Keyword misspelled or invalid format, [(D) TOPOLOGY:]
 L:499 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
 L:510 M:220 C: Keyword misspelled or invalid format, [(C) STRANDEDNESS:]
 L:511 M:220 C: Keyword misspelled or invalid format, [(D) TOPOLOGY:]
 L:515 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
 L:531 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
 L:550 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
 L:552 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14